

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
Racie, Lisa A.  
LaVallie, Edward R.  
Merberg, David  
Treacy, Maurice  
Evans, Cheryl  
Agostino, Michael  
Lu, Zhijian  
Honjo, Tasuku  
Tashiro, Kei  
Nakamura, Tomoyuki
- (ii) TITLE OF INVENTION: SECRETED PROTEINS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: MA
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sprunger, Suzanne A.
  - (B) REGISTRATION NUMBER: P-41,323
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8284
  - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAGCTTGGCA	CGAGGGGACC	CCGGCGCTCT	CCCCGTGTCC	TCTCCACGAC	TCGCTCGGCC	60
CCTCTGGAAT	AAAACACCCG	CGAGCCCCGA	GGGCCCAGAG	GAGGCCGACG	TGCCCCGAGCT	120
CCTCCGGGGG	TCCCGCCCGC	GAGCTTTCTT	CTCGCCTTCG	CATCTCCTCC	TCGCGCGTCT	180
TGGACATGCC	AGGAATAAAA	AGGATACTCA	CTGTTACCAT	TCTGGCTCTC	TGTCTTCCAA	240
GCCCTGGGAA	TGCACAGGCA	CAGTGCACGA	ATGGCTTTGA	CCTGGATCGC	CAGTCAGGAC	300
AGTGTTTAGA	TATTGATGAA	TGCCGAACCA	TCCCCGAGGC	CTGCCGAGGA	GACATGATGT	360
GTGTTAACCA	AAATGGCGGG	TATTTATGCA	TTCCCCGAC	AAACCTGTG	TATCGAGGGC	420
CCTACTCGAA	CCCCTACTCG	ACCCCTACT	CAGGTCCGTA	CCCAGCAGCT	GCCCCACCAC	480
TCTCAGCTCC	AAACTATCCC	ACGATCTCCA	GGCCTCTTAT	ATGCCGCTTT	GGATACCAGA	540
TGGATGAAAG	CAACCAATGT	GTGGATGTGG	ACGAGTGTGC	AACAGATTCC	CACCACTGCA	600
ACCCACCCA	GATCTGCATC	AATACTGAAG	GCGGGTACAC	CTGCTCCTGC	ACCGACGGAT	660
ATTGGCTTCT	GGAAGGCCAG	TGCTTAGACA	TTGATGAATG	TCGCTATGGT	TACTGCCAGC	720
AGCTCTGTGC	GAATGTTCCCT	GGATCCTATT	CTGTACATG	CAACCTGGT	TTTACCCTCA	780
ATGAGGATGG	AAGGTCTTGC	CAAGATGTGA	ACGAGTGTGC	CACCGAGAAC	CCCTGCGTGC	840
AAACCTGCGT	CAACACCTAC	GGCTCTTTCA	TCTGCCGCTG	TGACCCAGGA	TATGAACTTG	900
AGGAAGATGG	CGTTCATTGC	AGTGATATGG	ACGAGTGCAG	CTTCTCTGAG	TTCTCTGCC	960
AACATGAGTG	TGTGAACCAG	CCCGGCACAT	ACTTCTGCTC	CTGCCCTCCA	GGCTACATCC	1020
TGCTGGATGA	CAACCGAAGC	TGCCAAGACA	TCAACGAATG	TGAGCACAGG	AACCACACGT	1080
GCAACCTGCA	GCAGACGTGC	TACAATTTAC	AAGGGGGCTT	CAAATGCATC	GACCCCATCC	1140
GCTGTGAGGA	GCCTTATCTG	AGGATCAGTG	ATAACCGCTG	TATGTGTCCT	GCTGAGAACC	1200
CTGGCTGCAG	AGACCAGCCC	TTTACCATCT	TGTACCGGGA	CATGGACGTG	GTGTCAGGAC	1260
GCTCCGTTCC	CGCTGACATC	TTCCAAATGC	AAGCCACGAC	CCGCTACCCT	GGGGCCTATT	1320
ACATTTTCCA	GATCAAATCT	GGGAATGAGG	GCAGAGAATT	TTACATGCGG	CAAACGGGCC	1380
CCATCAGTGC	CACCTGGTG	ATGACACGCC	CCATCAAAGG	GCCCCGGGAA	ATCCAGCTGG	1440
ACTTGAAAT	GATCACTGTC	AACACTGTCA	TCAACTTCAG	AGGCAGCTCC	GTGATCCGAC	1500
TGCGGATATA	TGTGTCGCAG	TACCCATTCT	GAGCCTCGGG	CTGGAGCCTC	CGACGCTGCC	1560
TCTCATTGGC	ACCAAGGGAC	AGGAGAAGAG	AGGAAATAAC	AGAGAGAATG	AGAGCGACAC	1620
AGACGTTAGG	CATTTCTGTC	TGAACGTTTC	CCCGAAGAGT	CAGCCCCGAC	TTCCTGACTC	1680
TCACCTGTAC	TATTGCAGAC	CTGTCACCTT	GCAGGACTTG	CCACCCCCAG	TTCCTATGAT	1740
ACAGTTATCA	AAAAGTATTA	TCATTGCTCC	CCTGATAGAA	GATTGTTGGT	GAATTTTCAA	1800
GGCCTTCAGT	TTATTTCCAC	TATTTTCAAA	GAAAATAGAT	TAGGTTTTCG	GGGGTCTGAG	1860
TCTATGTTCA	AAGACTGTGA	ACAGCTTGCT	GTCACTTCTT	CACCTCTTCC	ACTCCTTCTC	1920

TCACTGTGTT ACTGCTTTGC AAAGACCCGG GAGCTGGCGG GGAACCCTGG GAGTAGCTAG 1980  
 TTTGCTTTTT GCGTACACAG AGAAGGCTAT GTAAACAAAC CACAGCAGGA TCGAAGGGTT 2040  
 TTTAGAGAAT GTGTTTCAAA ACCATGCCTG GTATTTTCAA CCATAAAAGA AGTTTCAGTT 2100  
 GTCCTTAAAT TTGTATAACG GTTTAATTCT GTCTTGTTCA TTTTGAGTAT TTTTAAAAAA 2160  
 TATGTCGTAG AATTCCTTCG AAAGGCCTTC AGACACATGC TATGTTCTGT CTTCCCAAAC 2220  
 CCAGTCTCCT CTCCATTTTA GCCCAGTGTT TTCTTTGAGG ACCCCTTAAT CTTGCTTTCT 2280  
 TTAGAATTTT TACCCAATTG GATTGGAATG CAGAGGTCTC CAAACTGATT AAATATTTGA 2340  
 AGAGAAAAAA AAAAAAAAAA AA 2362

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 448 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gly	Ile	Lys	Arg	Ile	Leu	Thr	Val	Thr	Ile	Leu	Ala	Leu	Cys	1	5	10	15
Leu	Pro	Ser	Pro	Gly	Asn	Ala	Gln	Ala	Gln	Cys	Thr	Asn	Gly	Phe	Asp	20	25	30	
Leu	Asp	Arg	Gln	Ser	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Thr	35	40	45	
Ile	Pro	Glu	Ala	Cys	Arg	Gly	Asp	Met	Met	Cys	Val	Asn	Gln	Asn	Gly	50	55	60	
Gly	Tyr	Leu	Cys	Ile	Pro	Arg	Thr	Asn	Pro	Val	Tyr	Arg	Gly	Pro	Tyr	65	70	75	80
Ser	Asn	Pro	Tyr	Ser	Thr	Pro	Tyr	Ser	Gly	Pro	Tyr	Pro	Ala	Ala	Ala	85	90	95	
Pro	Pro	Leu	Ser	Ala	Pro	Asn	Tyr	Pro	Thr	Ile	Ser	Arg	Pro	Leu	Ile	100	105	110	
Cys	Arg	Phe	Gly	Tyr	Gln	Met	Asp	Glu	Ser	Asn	Gln	Cys	Val	Asp	Val	115	120	125	
Asp	Glu	Cys	Ala	Thr	Asp	Ser	His	Gln	Cys	Asn	Pro	Thr	Gln	Ile	Cys	130	135	140	
Ile	Asn	Thr	Glu	Gly	Gly	Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp	145	150	155	160
Leu	Leu	Glu	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly	Tyr	165	170	175	

Asn	Pro	Gly	Phe	Thr	Leu	Asn	Glu	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val
		195					200					205			
Asn	Glu	Cys	Ala	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr
		210					215				220				
Tyr	Gly	Ser	Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu
225					230					235					240
Asp	Gly	Val	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu	Phe
				245					250					255	
Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Thr	Tyr	Phe	Cys	Ser
			260					265					270		
Cys	Pro	Pro	Gly	Tyr	Ile	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp
		275					280					285			
Ile	Asn	Glu	Cys	Glu	His	Arg	Asn	His	Thr	Cys	Asn	Leu	Gln	Gln	Thr
		290				295					300				
Cys	Tyr	Asn	Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Arg	Cys
305					310					315					320
Glu	Glu	Pro	Tyr	Leu	Arg	Ile	Ser	Asp	Asn	Arg	Cys	Met	Cys	Pro	Ala
				325					330					335	
Glu	Asn	Pro	Gly	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp
			340					345					350		
Met	Asp	Val	Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	Ile	Phe	Gln	Met
		355					360					365			
Gln	Ala	Thr	Thr	Arg	Tyr	Pro	Gly	Ala	Tyr	Tyr	Ile	Phe	Gln	Ile	Lys
		370				375					380				
Ser	Gly	Asn	Glu	Gly	Arg	Glu	Phe	Tyr	Met	Arg	Gln	Thr	Gly	Pro	Ile
385					390					395					400
Ser	Ala	Thr	Leu	Val	Met	Thr	Arg	Pro	Ile	Lys	Gly	Pro	Arg	Glu	Ile
				405					410					415	
Gln	Leu	Asp	Leu	Glu	Met	Ile	Thr	Val	Asn	Thr	Val	Ile	Asn	Phe	Arg
			420					425					430		
Gly	Ser	Ser	Val	Ile	Arg	Leu	Arg	Ile	Tyr	Val	Ser	Gln	Tyr	Pro	Phe
		435					440					445			